



sequence listing.ST25  
SEQUENCE LISTING

<110> Wei, Guangwen  
Guo, Rongbing  
Zhang, Renhuai

<120> Recombinant Super-Compound Interferon

<130> 792-A-PCT-US

<140> 10/650,365

<141> 2003-08-28

<150> PCT/CN02/00128

<151> 2002-02-28

<150> CN 01104367.9

<151> 2001-02-28

<160> 13

<170> PatentIn version 3.2

<210> 1

<211> 504

<212> DNA

<213> human synthesis

<220>

<221> CDS

<222> (1)..(504)

<400> 1

atg	tgc	gac	ctg	ccg	cag	acc	cac	tcc	ctg	ggc	aac	cgt	cgt	gct	ctg	48
Met	Cys	Asp	Leu	Pro	Gln	Thr	His	Ser	Leu	Gly	Asn	Arg	Arg	Ala	Leu	
1				5					10					15		

atc	ctg	ctg	gct	cag	atg	cgt	cgt	atc	tcc	ccg	ttc	tcc	tgc	ctg	aaa	96
Ile	Leu	Leu	Ala	Gln	Met	Arg	Arg	Ile	Ser	Pro	Phe	Ser	Cys	Leu	Lys	
			20					25					30			

gac	cgt	cac	gac	ttc	ggc	ttc	ccg	cag	gaa	gaa	ttc	gac	ggc	aac	cag	144
Asp	Arg	His	Asp	Phe	Gly	Phe	Pro	Gln	Glu	Glu	Phe	Asp	Gly	Asn	Gln	
		35					40					45				

ttc	cag	aaa	gct	cag	gct	atc	tcc	gtt	ctg	cac	gaa	atg	atc	cag	cag	192
Phe	Gln	Lys	Ala	Gln	Ala	Ile	Ser	Val	Leu	His	Glu	Met	Ile	Gln	Gln	
	50					55					60					

acc	ttc	aac	ctg	ttc	tcc	acc	aaa	gac	tcc	tcc	gct	gct	tgg	gac	gaa	240
Thr	Phe	Asn	Leu	Phe	Ser	Thr	Lys	Asp	Ser	Ser	Ala	Ala	Trp	Asp	Glu	
65					70					75					80	

tcc	ctg	ctg	gaa	aaa	ttc	tac	acc	gaa	ctg	tac	cag	cag	ctg	aac	gac	288
Ser	Leu	Leu	Glu	Lys	Phe	Tyr	Thr	Glu	Leu	Tyr	Gln	Gln	Leu	Asn	Asp	
				85					90					95		

ctg	gaa	gct	tgc	gtt	atc	cag	gaa	gtt	ggc	gtt	gaa	gaa	acc	ccg	ctg	336
Leu	Glu	Ala	Cys	Val	Ile	Gln	Glu	Val	Gly	Val	Glu	Glu	Thr	Pro	Leu	
			100					105					110			

atg	aac	gtt	gac	tcc	atc	ctg	gct	gtt	aaa	aaa	tac	ttc	cag	cgt	atc	384
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Met	Asn	Val	Asp	Ser	Ile	Leu	Ala	Val	Lys	Lys	Tyr	Phe	Gln	Arg	Ile	
		115					120					125				
acc	ctg	tac	ctg	acc	gaa	aaa	aaa	tac	tcc	ccg	tgc	gct	tgg	gaa	gtt	432
Thr	Leu	Tyr	Leu	Thr	Glu	Lys	Lys	Tyr	Ser	Pro	Cys	Ala	Trp	Glu	Val	
		130				135					140					
gtt	cgt	gct	gaa	atc	atg	cgt	tcc	ttc	tcc	ctg	tcc	acc	aac	ctg	cag	480
Val	Arg	Ala	Glu	Ile	Met	Arg	Ser	Phe	Ser	Leu	Ser	Thr	Asn	Leu	Gln	
		145			150					155					160	
gaa	cgt	ctg	cgt	cgt	aaa	gaa	taa									504
Glu	Arg	Leu	Arg	Arg	Lys	Glu										
				165												

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 <213> human synthesis  
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Met	Cys	Asp	Leu	Pro	Gln	Thr	His	Ser	Leu	Gly	Asn	Arg	Arg	Ala	Leu
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			20					25					30		
Asp	Arg	His	Asp	Phe	Gly	Phe	Pro	Gln	Glu	Glu	Phe	Asp	Gly	Asn	Gln
		35					40					45			
Phe	Gln	Lys	Ala	Gln	Ala	Ile	Ser	Val	Leu	His	Glu	Met	Ile	Gln	Gln
		50				55					60				
Thr	Phe	Asn	Leu	Phe	Ser	Thr	Lys	Asp	Ser	Ser	Ala	Ala	Trp	Asp	Glu
					70					75					80
Ser	Leu	Leu	Glu	Lys	Phe	Tyr	Thr	Glu	Leu	Tyr	Gln	Gln	Leu	Asn	Asp
				85					90					95	
Leu	Glu	Ala	Cys	Val	Ile	Gln	Glu	Val	Gly	Val	Glu	Glu	Thr	Pro	Leu
			100					105					110		
Met	Asn	Val	Asp	Ser	Ile	Leu	Ala	Val	Lys	Lys	Tyr	Phe	Gln	Arg	Ile
		115					120					125			
Thr	Leu	Tyr	Leu	Thr	Glu	Lys	Lys	Tyr	Ser	Pro	Cys	Ala	Trp	Glu	Val
		130				135					140				
Val	Arg	Ala	Glu	Ile	Met	Arg	Ser	Phe	Ser	Leu	Ser	Thr	Asn	Leu	Gln
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Glu Arg Leu Arg Arg Lys Glu  
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<211> 360  
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<220>  
<221> CDS  
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att ctg ctg gca cag atg cgt cgt att tcc ccg ttt agc tgc ctg aaa 96  
Ile Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys  
20 25 30  
gac cgt cac gac ttc ggc ttt ccg caa gaa gag ttc gat ggc aac caa 144  
Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln  
35 40 45  
ttc cag aaa gct cag gca atc tct gta ctg cac gaa atg atc caa cag 192  
Phe Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln  
50 55 60  
acc ttc aac ctg ttt tcc act aaa gac agc tct gct gct tgg gac gaa 240  
Thr Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu  
65 70 75 80  
agc ttg ctg gag aag ttc tac act gaa ctg tat cag cag ctg aac gac 288  
Ser Leu Leu Glu Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp  
85 90 95  
ctg gaa gca tgc gta atc cag gaa gtt ggt gta gaa gag act ccg ctg 336  
Leu Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu  
100 105 110  
atg aac gtc gac tct att ctg gca 360  
Met Asn Val Asp Ser Ile Leu Ala  
115 120

<210> 4  
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<212> PRT  
<213> human synthesis

<400> 4  
Met Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu  
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Ile Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys  
20 25 30

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Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln  
35 40 45

Phe Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln  
50 55 60

Thr Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu  
65 70 75 80

Ser Leu Leu Glu Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp  
85 90 95

Leu Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu  
100 105 110

Met Asn Val Asp Ser Ile Leu Ala  
115 120

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<222> (1)..(108)

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1 5 10 15  
atc ctg ctg gct cag atg cgt cgt atc tcc ccg ttc tcc tgc ctg aaa 96  
Ile Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys  
20 25 30  
gac cgt cac gac 108  
Asp Arg His Asp  
35

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Met Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu  
1 5 10 15  
Ile Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys  
20 25 30

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aagctcaggc tatctccggt ctgcacgaaa tgatccagca gaccttc 107

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<222> (1)..(103)  
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gctgctggtg cagttcgggt tagaattttt ccagcagggg ttcgtcccaa gcagcggagg 60  
agtctttggt ggagaacagg ttgaaggtct gctggatcat ttc 103

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atccctgctg gaaaaattct acaccgaact gtaccagcag ctgaacgacc tggaagcttg 60  
cgttatccag gaagttggtg ttgaagaaac cccgctgatg aac 103

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gaagaaaccc cgctgatgaa cgttgactcc atcctggctg ttaaaaaata cttccagcgt 60  
atcacctgt acctgaccga aaaaaaatac tccccgtgcg cttggg 106

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